

re-run

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/803,055
Source: 1fw0
Date Processed by STIC: 3/31/04

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/803,055

DATE: 03/03/2005
TIME: 09:31:38

Input Set : N:\AMC\US10803055.raw
Output Set: N:\CRF4\03032005\J803055.raw

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1 <110> APPLICANT: Universite de Liege
2 <120> TITLE OF INVENTION: Cold-active beta galactosidase, the process for its
3 preparation and the use thereof
4 <130> FILE REFERENCE: Beta-gal
5 <140> CURRENT APPLICATION NUMBER: US/10/803,055
6 <141> CURRENT FILING DATE: 2004-03-18
7 <150> PRIOR APPLICATION NUMBER: US/09/501,136
8 <151> PRIOR FILING DATE: 2000-02-09
9 <160> NUMBER OF SEQ ID NOS: 2
10 <170> SOFTWARE: PatentIn Ver. 2.1
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 3171
14 <212> TYPE: DNA
15 <213> ORGANISM: Pseudoalteromonas haloplanktis
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19 gtaaaagcac atagcccaact taacggcttt aaaacaattg aagacgcccgg taaaaataca 180
20 cagtcgcaga agaaaagttt aaacggggcag tgggattttt aattatttga taagcccgaa 240
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23 gttaaataacc catttgcagt aaacccgcca tttgtaccaa ggcataaccc tactggttgt 420
24 taccgcactg aatttacaat cacacctgag cagttaacgc agcgtAACCA tataattttt 480
25 gaaggcgtta actcggttt tcatctttgg tggtaacgggc agtgggtggg gtattcacaa 540
26 gatagccgct taccgagcga atttgattt agtgagctt tagttgtcggt tactaaccgt 600
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28 tggcttaagcg gtatttttcg cgatgttaac ttacttacaa aaccgcaaaag ccaaataacgc 720
29 gatgtgttta taaccccgaa ttttagacgt tgctatcgat atgcaacgct acatataaaa 780
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31 tcactgtgcg agccaaaaat tcaaaggact aacaataaac gtgttgatga aaaagggggg 900
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42 caatacgggg gccgcgggtgc aaacacgaca gctaccgata ttatggccc aatgtactcc 1560
43 cgttagata ccgatattaa agacgatgcg gtacctaagt attcaattaa aaaatggctg 1620
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47 tattggcgtt acggcggcga ctgggtgtt gaactaaacg accggcagtt ttgtataaac 1860
48 ggcttattgt tcccgatcg tacaccgtt cctagccat ttgaagctaa atacagccag 1920
49 caacatttac aatttacact gcgcgagcaa aatcaaaaatc aaaaccaaaa ccaatacagc 1980
50 attgatgtat ttagcgat ttagtattttt cacaccgata acgaaaaact cgttggcaa 2040
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67 aaacacacta acgaactaat tgctgtatgat tgcatatttgcgatcatcaacat 3060
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71 <210> SEQ ID NO: 2
72 <211> LENGTH: 1039
73 <212> TYPE: PRT
74 <213> ORGANISM: Pseudoalteromonas haloplanktis
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76 <221> NAME/KEY: ACT_SITE
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78 <220> FEATURE:
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93 <400> SEQUENCE: 2
94 Met Thr Ser Leu Gln His Ile Ile Asn Arg Arg Asp Trp Glu Asn Pro

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95	1	5	10	15
96	Ile Thr Val Gln Val Asn Gln Val Lys Ala His Ser Pro Leu Asn Gly			
97	20	25	30	
98	Phe Lys Thr Ile Glu Asp Ala Arg Glu Asn Thr Gln Ser Gln Lys Lys			
99	35	40	45	
100	Ser Leu Asn Gly Gln Trp Asp Phe Lys Leu Phe Asp Lys Pro Glu Ala			
101	50	55	60	
102	Val Asp Glu Ser Leu Leu Tyr Glu Lys Ile Ser Lys Glu Leu Ser Gly			
103	65	70	75	80
104	Asp Trp Gln Ser Ile Thr Val Pro Ser Asn Trp Gln Leu His Gly Phe			
105	85	90	95	
106	Asp Lys Pro Ile Tyr Cys Asn Val Lys Tyr Pro Phe Ala Val Asn Pro			
107	100	105	110	
108	Pro Phe Val Pro Ser Asp Asn Pro Thr Gly Cys Tyr Arg Thr Glu Phe			
109	115	120	125	
110	Thr Ile Thr Pro Glu Gln Leu Thr Gln Arg Asn His Ile Ile Phe Glu			
111	130	135	140	
112	Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Gln Trp Val Gly			
113	145	150	155	160
114	Tyr Ser Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Glu Leu			
115	165	170	175	
116	Leu Val Val Gly Thr Asn Arg Ile Ala Val Met Val Ile Arg Trp Ser			
117	180	185	190	
118	Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Trp Leu Ser Gly Ile			
119	195	200	205	
120	Phe Arg Asp Val Asn Leu Leu Thr Lys Pro Gln Ser Gln Ile Arg Asp			
121	210	215	220	
122	Val Phe Ile Thr Pro Asp Leu Asp Ala Cys Tyr Arg Asp Ala Thr Leu			
123	225	230	235	240
124	His Ile Lys Thr Ala Ile Asn Ala Pro Asn Asn Tyr Gln Val Ala Val			
125	245	250	255	
126	Gln Ile Phe Asp Gly Lys Thr Ser Leu Cys Glu Pro Lys Ile Gln Ser			
127	260	265	270	
128	Thr Asn Asn Lys Arg Val Asp Glu Lys Gly Gly Trp Ser Asp Val Val			
129	275	280	285	
130	Phe Gln Thr Ile Ala Ile Arg Ser Pro Lys Lys Trp Thr Ala Glu Thr			
131	290	295	300	
132	Pro Tyr Leu Tyr Arg Cys Val Val Ser Leu Leu Asp Glu Gln Gly Asn			
133	305	310	315	320
134	Thr Val Asp Val Glu Ala Tyr Asn Ile Gly Phe Arg Lys Val Glu Met			
135	325	330	335	
136	Leu Asn Gly Gln Leu Cys Val Asn Gly Lys Pro Leu Leu Ile Arg Gly			
137	340	345	350	
138	Val Asn Arg His Glu His His Pro Glu Asn Gly His Ala Val Ser Thr			
139	355	360	365	
140	Ala Asp Met Ile Glu Asp Ile Lys Leu Met Lys Gln Asn Asn Phe Asn			
141	370	375	380	
142	Ala Val Arg Thr Ala His Tyr Pro Asn His Pro Leu Phe Tyr Glu Leu			
143	385	390	395	400

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144 Cys Asp Glu Leu Gly Leu Tyr Val Val Asp Glu Ala Asn Ile Glu Thr
 145 405 410 415
 146 His Gly Met Phe Pro Met Gly Arg Leu Ala Ser Asp Pro Leu Trp Ala
 147 420 425 430
 148 Gly Ala Phe Met Ser Arg Tyr Thr Gln Met Val Glu Arg Asp Lys Asn
 149 435 440 445
 150 His Ala Ser Ile Ile Trp Ser Leu Gly Asn Glu Cys Gly His Gly
 151 450 455 460
 152 Ala Asn His Asp Ala Met Tyr Gly Trp Ser Lys Ser Phe Asp Pro Ser
 153 465 470 475 480
 154 Arg Pro Val Gln Tyr Glu Gly Gly Ala Asn Thr Thr Ala Thr Asp
 155 485 490 495
 156 Ile Ile Cys Pro Met Tyr Ser Arg Val Asp Thr Asp Ile Lys Asp Asp
 157 500 505 510
 158 Ala Val Pro Lys Tyr Ser Ile Lys Lys Trp Leu Ser Leu Pro Gly Glu
 159 515 520 525
 160 Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly Asn Ser
 161 530 535 540
 162 Leu Gly Ser Phe Asp Asp Tyr Trp Gln Ala Phe Arg Glu Tyr Pro Arg
 163 545 550 555 560
 164 Leu Gln Gly Gly Phe Ile Trp Asp Trp Val Asp Gln Gly Leu Ser Lys
 165 565 570 575
 166 Ile Asp Glu Asn Gly Lys His Tyr Trp Ala Tyr Gly Gly Asp Phe Gly
 167 580 585 590
 168 Asp Glu Leu Asn Asp Arg Gln Phe Cys Ile Asn Gly Leu Leu Phe Pro
 169 595 600 605
 170 Asp Arg Thr Pro His Pro Ser Leu Phe Glu Ala Lys Tyr Ser Gln Gln
 171 610 615 620
 172 His Leu Gln Phe Thr Leu Arg Glu Gln Asn Gln Asn Gln Asn
 173 625 630 635 640
 174 Gln Tyr Ser Ile Asp Val Phe Ser Asp Tyr Val Phe Arg His Thr Asp
 175 645 650 655
 176 Asn Glu Lys Leu Val Trp Gln Leu Ile Gln Asn Gly Val Cys Val Glu
 177 660 665 670
 178 Gln Gly Glu Met Ala Leu Asn Ile Ala Pro Gln Ser Thr His Thr Leu
 179 675 680 685
 180 Thr Ile Lys Thr Lys Thr Ala Phe Glu His Gly Ala Gln Tyr Tyr Leu
 181 690 695 700
 182 Asn Leu Asp Val Ala Leu Ile Asn Asp Ser His Phe Ala Asn Ala Asn
 183 705 710 715 720
 184 His Val Met Asp Ser Glu Gln Phe Lys Leu Ile Asn Ser Asn Asn Leu
 185 725 730 735
 186 Asn Ser Lys Ser Phe Ala Ser Ala Thr Glu Lys Ser Val Ile Ser Val
 187 740 745 750
 188 Asn Glu Thr Asp Ser His Leu Ser Ile Glu Asn Asn Thr Phe Lys Leu
 189 755 760 765
 190 Val Phe Asn Gln Gln Ser Gly Leu Ile Glu Gln Trp Leu Gln Asp Asp
 191 770 775 780
 192 Thr Gln Val Ile Ser Ser Pro Leu Val Asn Phe Tyr Arg Ala Pro

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195	805	810	815	
196	Ala Trp Glu Ala Arg Trp Ser Arg Ala Gly Ile Gly Gln Trp Gln Arg			
197	820	825	830	
198	Thr Cys Ser Ser Ile Asn Ala Val Gln Ser Ser Val Asp Val Arg Ile			
199	835	840	845	
200	Thr Cys Val Phe Asn Tyr Glu Phe Asn Gly Val Leu Gln Ala Gln Thr			
201	850	855	860	
202	Gln Trp Leu Tyr Thr Leu Asn Asn Thr Gly Thr Ile Ser Leu Asn Val			
203	865	870	875	880
204	Asp Val Asn Leu Asn Asp Thr Leu Pro Pro Met Pro Arg Ile Gly Leu			
205	885	890	895	
206	Ser Thr Thr Ile Asn Lys Gln Ser Asp Thr Lys Val Asn Trp Leu Gly			
207	900	905	910	
208	Leu Gly Pro Phe Glu Asn Tyr Pro Asp Arg Lys Ser Ala Ala Arg Phe			
209	915	920	925	
210	Gly Tyr Tyr Ser Leu Ser Leu Asn Glu Leu Tyr Thr Pro Tyr Ile Phe			
211	930	935	940	
212	Pro Thr Asp Asn Gly Leu Arg Ser Asp Cys Gln Leu Leu Ser Ile Asn			
213	945	950	955	960
214	Asn Leu Ile Val Thr Gly Ala Phe Leu Phe Ala Ala Ser Glu Tyr Ser			
215	965	970	975	
216	Gln Asn Met Leu Thr Gln Ala Lys His Thr Asn Glu Leu Ile Ala Asp			
217	980	985	990	
218	Asp Cys Ile His Val His Ile Asp His Gln His Met Gly Val Gly Gly			
219	995	1000	1005	
220	Asp Asp Ser Trp Ser Pro Ser Thr His Lys Glu Tyr Leu Leu Glu Gln			
221	1010	1015	1020	
222	Lys Asn Tyr Asn Tyr Ser Leu Thr Leu Thr Gly Gly Ile Thr Thr			
223	1025	1030	1035	

VERIFICATION SUMMARY

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